


  
1633

RAW SEQUENCE LISTING DATE: 06/21/2000  
 PATENT APPLICATION: US/09/451,291 TIME: 10:52:34

Input Set : A:\Sequence  
 Output Set: N:\CRF3\06212000\I451291.raw

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4 <110> APPLICANT: Chen, Lieping
6 <120> TITLE OF INVENTION: B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE
8 <130> FILE REFERENCE: 07039/187001
10 <140> CURRENT APPLICATION NUMBER: US 09/451,291
11 <141> CURRENT FILING DATE: 1999-11-30
13 <160> NUMBER OF SEQ ID NOS: 12
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 290
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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24 1 5 10 15
25 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
26 20 25 30
27 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
28 35 40 45
29 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
30 50 55 60
31 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
32 65 70 75 80
33 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
34 85 90 95
35 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
36 100 105 110
37 Arg Cys Met Ile Ser Tyr Gly Ala Asp Tyr Lys Arg Ile Thr Val
38 115 120 125
39 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
40 130 135 140
41 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
42 145 150 155 160
43 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
44 165 170 175
45 Gly Lys Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
46 180 185 190
47 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Asn Glu Ile Phe Tyr
48 195 200 205
49 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
50 210 215 220
51 Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
52 225 230 235 240
53 Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
54 245 250 255
55 Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
56 260 265 270
57 Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu

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TECH CENTER 1600/2900

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Input Set : A:\Sequence  
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Input Set : A:\Sequence  
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111	165	170	175
112 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val			
113	180	185	190
114 Thr Ser Ser Leu Arg Val Asn Ile Thr Ala Asn Asp Val Thr Tyr Cys			
115	195	200	205
116 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile			
117	210	215	220
118 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp			
119	225	230	235
120 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val			240
121	245	250	255
122 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys			
123	260	265	270
124 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu			
125	275	280	285
126 Glu Thr			
127	290		
129 <210> SEQ ID NO: 4			
130 <211> LENGTH: 873			
131 <212> TYPE: DNA			
132 <213> ORGANISM: Mus musculus			
134 <220> FEATURE:			
135 <221> NAME/KEY: CDS			
136 <222> LOCATION: (1)...(870)			
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139 atg agg ata ttt gct ggc att ata ttc aca gec tgc tgt cac ttg cta			48
140 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu			
141	1	5	10
143	15		
142 cgg gcg ttt act atc acg gct cca aag gac tac ttg tac gtg gtg gag tat			96
144 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr			
145	20	25	30
146	30		
147 ggc agc aac gtc acg atg gag tgc aga ttc cct gta gaa cgg gag ctg			144
148 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu			
149	35	40	45
150	45		
151 gac ctg ctt gcg tta gtg gtg tac tgg gaa aag gaa gat gag caa gtg			192
152 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val			
153	50	55	60
154	60		
155 att cag ttt gtg gca gga gag gag gac ctt aag cct cag cac agc aac			240
156 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn			
157	65	70	75
158	80		
159 ttc agg ggg aga gcc tcg ctc cca aag gac cag ctt ttg aag gga aat			288
160 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn			
161	85	90	95
162	95		
163 gct gcc ctt cag atc aca gac gtc aag ctg cag gac gca ggc gtt tac			336
164 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr			
165	100	105	110
166	110		
167 tgc tgc ata atc agc tac ggt ggt gcg gac tac aag cga atc acg ctg			384
168 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu			
169	115	120	125

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Input Set : A:\Sequence  
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171	aaa gtc aat gcc cca tac cgc aaa atc aac cag aga att tcc gtg gat	432
172	Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp	
173	130	135 140
175	ccc ccc act tat gag cat gag cta cta ttt ttt ctt ctt ctt cca	460
176	Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro	
177	145	150 155 160
179	gaa gct gag gta atc tgg aca aac agt gac cac caa ccc gtg agt ggg	528
180	Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly	
181	165	170 175
183	aag aga agt gtc acc act tcc cgg aca gag ggg atg ctt ctc aat gtg	576
184	Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val	
185	180	185 190
187	acc agc agt ctg agg gtc aac gcc aca gcg aat gat gtt ttc tac tgt	624
188	Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys	
189	195	200 205
191	acg ttt tgg aga tca cag cca ggg caa aac cac aca gcg gag ctg atc	672
192	Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile	
193	210	215 220
195	atc cca gaa ctg cct gca aca cat cct cca cag aac agg act cac tgg	720
196	Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp	
197	225	230 235 240
199	gtg ctt ctg gga tcc atc ctg ttg ttc ctc att gta gtg tcc acg gtc	768
200	Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val	
201	245	250 255
203	ctc ctc ttc ttg aga aaa caa gtg aga atg cta gat gtg gag aaa tgt	816
204	Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys	
205	260	265 270
207	ggc gtt gaa gat aca agc tca aaa aac cga aat gat aca caa ttc gag	864
208	Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu	
209	275	280 285
211	gag acg taa	873
212	Glu Thr	
213	290	
215	<210> SEQ ID NO: 5	
216	<211> LENGTH: 3616	
217	<212> TYPE: DNA	
218	<213> ORGANISM: Homo sapiens	
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221	<221> NAME/KEY: CDS	
222	<222> LOCATION: (73)...(942)	
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226	cattccagaa ag atg agg ata ttt gct gtc ttt ata ttc atg acc tac tgg	111
227	Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp	
228	1	5 10
230	cat ttg ctg aac gca ttt act gtc acg gtt ccc aag gac cta tat gtg	159
231	His Leu Leu Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val	
232	15	20 25
234	gta gag tat ggt agc aat atg aca att gaa tgc aaa ttc cca gta gaa	207

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235	Val	Glu	Tyr	Gly	Ser	Asn	Met	Thr	Ile	Glu	Cys	Lys	Phe	Pro	Val	Glu	
236	30																45
238	aaa	caa	tta	gac	ctg	gct	gca	cta	att	gtc	tat	tgg	gaa	atg	gag	gat	
239	Lys	Gln	Leu	Asp	Leu	Ala	Ala	Leu	Ile	Vai	Iyl	rrp	Glu	Met	Glu	Asp	
240																	60
242	aag	aac	att	att	caa	ttt	gtg	cat	gga	gag	gaa	gac	ctg	aag	gtt	cag	
243	Lys	Asn	Ile	Ile	Gln	Phe	Val	His	Gly	Glu	Glu	Asp	Leu	Lys	Val	Gln	
244																	75
246	cat	agt	agc	tac	aga	cag	agg	gcc	cg	ctg	ttg	aag	gac	cag	ctc	tcc	
247	His	Ser	Ser	Tyr	Arg	Gln	Arg	Ala	Arg	Leu	Leu	Lys	Asp	Gln	Leu	Ser	
248																	351
250	ctg	gga	aat	gct	gca	ctt	cag	atc	aca	gat	gtg	aaa	ttt	cag	gat	gca	
251	Leu	Gly	Asn	Ala	Ala	Leu	Gln	Ile	Thr	Asp	Val	Lys	Leu	Gln	Asp	Ala	
252																	399
254	ggg	gtg	tac	cgc	tgc	atg	atc	agc	tat	gtt	gtt	gcc	gac	tac	aag	cga	
255	Gly	Val	Tyr	Arg	Cys	Met	Ile	Ser	Tyr	Gly	Gly	Ala	Asp	Tyr	Lys	Arg	
256	110																447
258	att	act	gtg	aaa	gtc	aat	gcc	cca	tac	aac	aaa	atc	aac	caa	aga	att	
259	Ile	Thr	Val	Lys	Val	Asn	Ala	Pro	Tyr	Asn	Lys	Ile	Asn	Gln	Arg	Ile	
260																	495
262	ttg	gtg	gtt	cca	gtc	acc	tct	gaa	cat	gtt	aca	tgt	cag	gct			543
263	Leu	Val	Val	Asp	Pro	Val	Thr	Ser	Glu	His	Glu	Leu	Thr	Cys	Gln	Ala	
264																	543
266	gag	ggc	tac	ccc	aag	gcc	gaa	gtc	atc	tgg	aca	agc	agt	gac	cat	caa	
267	Glu	Gly	Tyr	Pro	Lys	Ala	Glu	Val	Ile	Trp	Thr	Ser	Ser	Asp	His	Gln	
268																	591
270	gtc	ctg	agt	ggt	aag	acc	acc	acc	acc	aat	tcc	aag	aga	gag	gag	aag	
271	Val	Leu	Ser	Gly	Lys	Thr	Thr	Thr	Asn	Ser	Lys	Arg	Glu	Glu	Lys		
272																	639
274	ttt	tcc	aat	gtg	acc	agc	aca	ctg	aga	atc	aaa	aca	aca	act	aat	gag	
275	Leu	Phe	Asn	Val	Thr	Ser	Thr	Leu	Arg	Ile	Asn	Thr	Thr	Asn	Glu		
276	190																687
278	att	tcc	tac	tgc	act	ttt	agg	aga	tta	gat	cct	gag	gaa	aac	cat	aca	
279	Ile	Phe	Tyr	Cys	Thr	Phe	Arg	Arg	Leu	Asp	Pro	Glu	Glu	Asn	His	Thr	
280																	735
282	gtt	gaa	ttt	gtc	atc	cca	gaa	cta	cct	gtg	gca	cat	cct	cca	aat	gaa	
283	Ala	Glu	Leu	Val	Ile	Pro	Glu	Leu	Pro	Leu	Ala	His	Pro	Pro	Asn	Glu	
284																	783
286	agg	act	cac	ttt	gtt	ata	ctg	ggg	gcc	atc	tta	tta	tgc	ctt	ggt	gtt	
287	Arg	Thr	His	Leu	Val	Ile	Leu	Gly	Ala	Ile	Leu	Leu	Cys	Leu	Gly	Val	
288																	831
290	gca	ctg	aca	ttc	atc	ttc	cgt	tta	aga	aaa	ggg	aga	atg	atg	gtt	gtt	
291	Ala	Leu	Thr	Phe	Ile	Phe	Arg	Leu	Arg	Lys	Gly	Arg	Met	Met	Asp	Val	
292																	879
294	aaa	aaa	tgt	ggc	atc	caa	gat	aca	aac	tca	aag	aag	caa	agt	gat	aca	
295	Lys	Lys	Cys	Gly	Ile	Gln	Asp	Thr	Asn	Ser	Lys	Lys	Gln	Ser	Asp	Thr	
296	270																927
298	cat	ttt	gag	gag	acg	taatccagca	tttggaaacctc										
299	His	Leu	Glu	Thr													982

**VERIFICATION SUMMARY** DATE: 06/21/2000  
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